

Replace the paragraph beginning at page 38, line 17, with the following rewritten paragraph:

FI
The term "core domain" (also referred to herein as "core") refers to the evolutionarily conserved domains of Sir2 or Sir2-like proteins which can be identified, for example, by the comparison of amino acid sequences by, for example, CLUSTAL X, BLAST, PSI-BLAST or FASTA algorithms. The "core domain" is the domain that shows significant identity and/or homology to about 240-270 amino acids of Sir2 or Sir2-like proteins (about 20-50% or higher as amino acid identity, see Figure 2) and/or possesses the consensus sequence GAG(V/I)S(T/V)S(L/C/A)GIPDFRS (SEQ ID NO:38) and YTQNID (SEQ ID NO: 28) (Brachmann, *et al.*, *Genes & Development* 9:2888-2902, (1995)). The "core domain" of Sir2 proteins has NAD-dependent deacetylation and/or mono-ADP-ribosylation activities. Any protein with a "core domain" of a Sir2 protein, a fragment of the core domain, or any functional or structural equivalent which is capable of NAD-dependent deacetylation and/or mono-ADP-ribosylation of nuclear proteins is within the scope of the invention.--